

FIG. 1A

SIGNAL CLEAVAGE SITE

MCKFTVVAALLLLGAVRAE-GSS-

LGGDLA-PQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACG-MQPARTPCTS-

PQPQKPQPQPQPQPQKPEPE-GTGSSE-KDEL

FIG. 1B

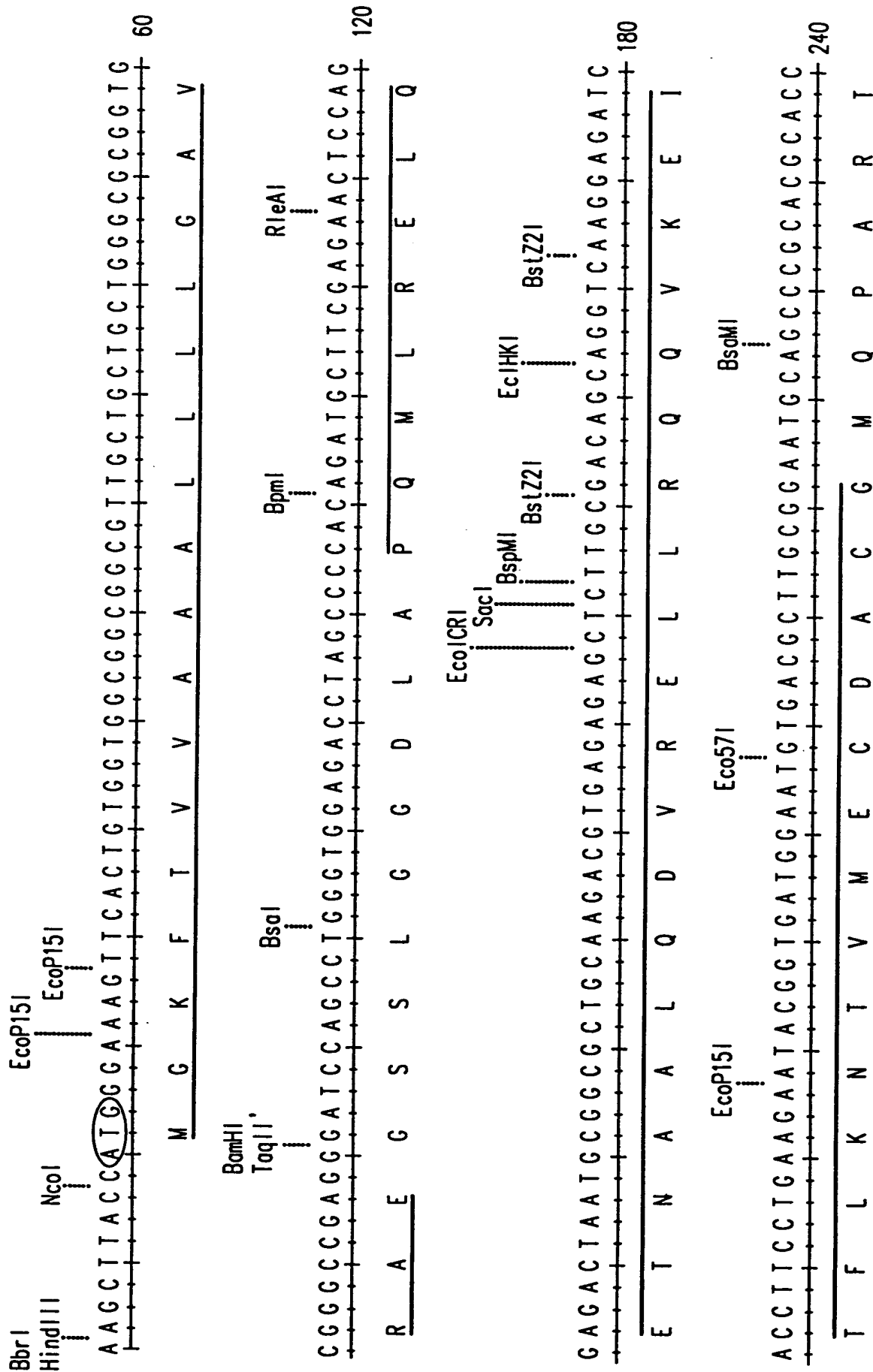


FIG. 1C

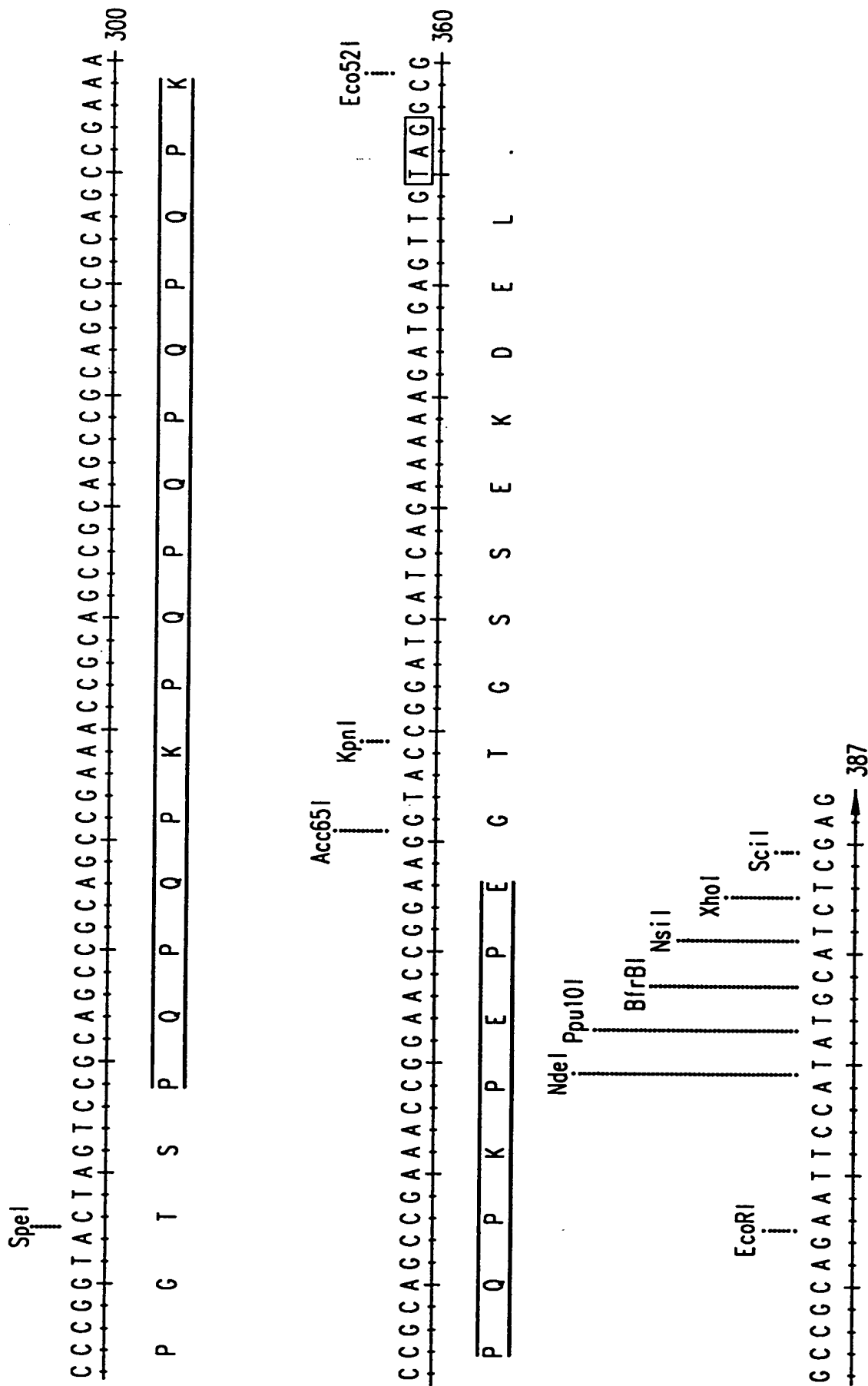


FIG. 1D

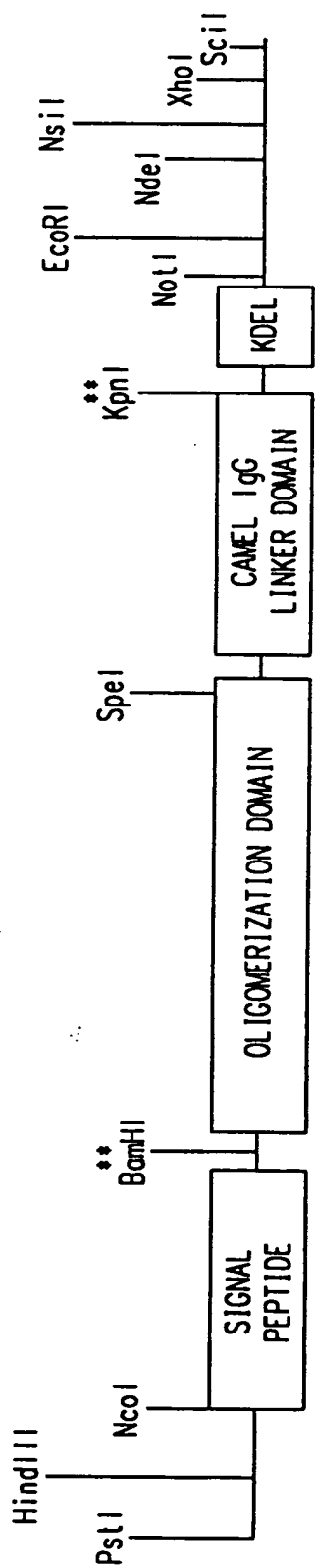


FIG. 2A

SIGNAL CLEAVAGE SITE

MGKFTVVAALLLGAVRAE-GSS-

LGGDCC-PQMLRELQETNAALQDVRELLRQQVKEITFLKNTVMECDACG-MQPARTPGTS-

PQPQKPQPQPQPQPQKPEPE-GTGSSE-KDEL

FIG. 2B

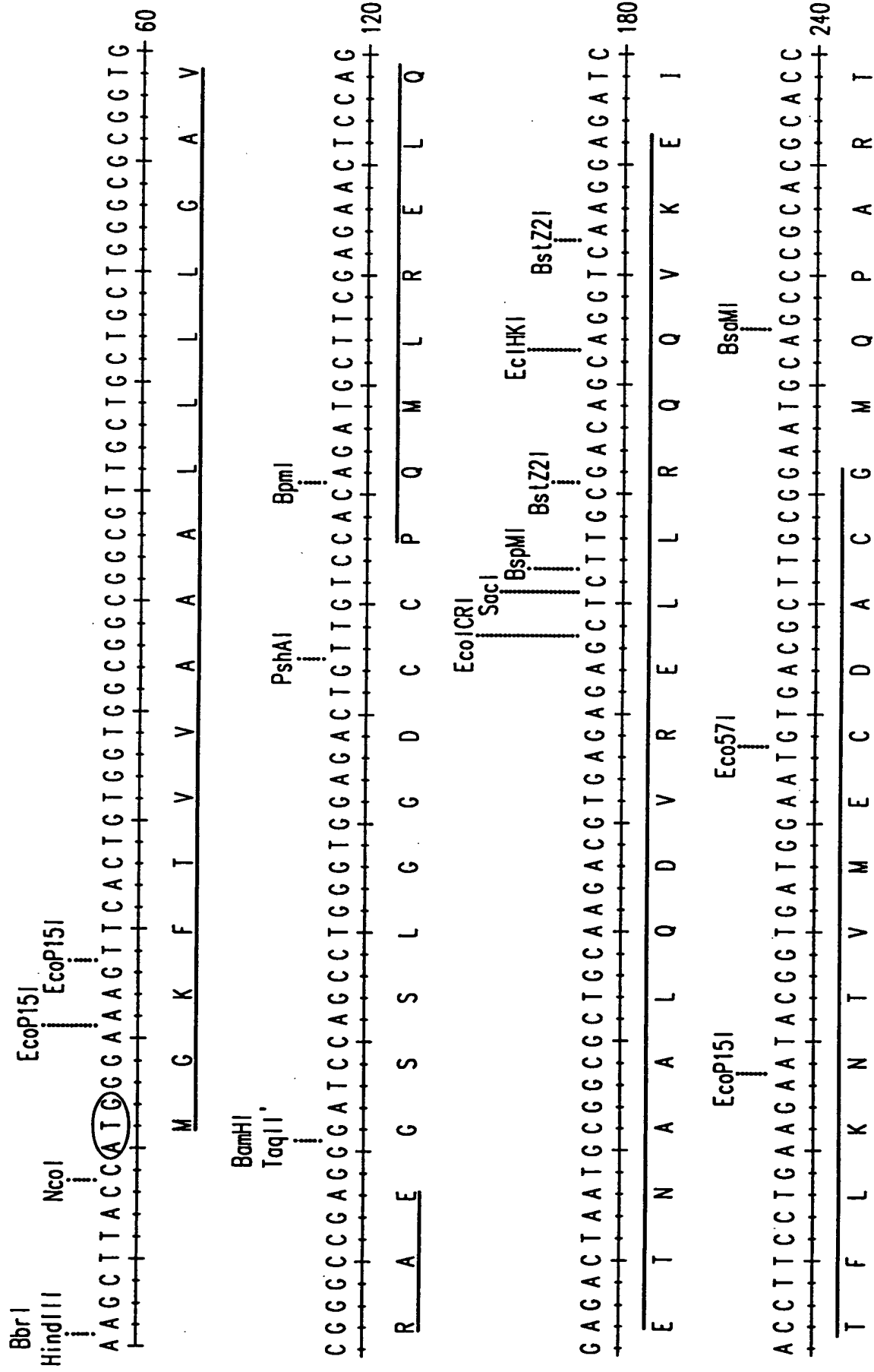


FIG. 2C

SpeI  
 ↓  
 C C C G T A C T A G T C C G C A G C C G C A A C C G C A G C C G C A G C C G C A G C C G A A 300

P	C	T	S
P	Q	P	Q
P	Q	P	K
P	Q	P	Q
P	Q	P	Q
P	Q	P	Q
P	Q	P	K

CCGCAGCCGAAACCCGGAACCCGGAAGGTACCCGGATCATCAGAAAGAATGAGTGTAGCCG  
 360  
 Eco52I  
 KpnI  
 Acc65I

P Q P K P E P E      G T G S S E K D E L

Restriction map of the 387 bp DNA fragment. The map shows the following restriction sites from left to right: NdeI, Ppu10I, BfrBI, NsiI, XhoI, EcoRI, and SclI. The DNA sequence is G C C C G A G A A T T C C A T A T G C A T C T C G A G. The fragment size is 387 bp.

**FIG. 2D**



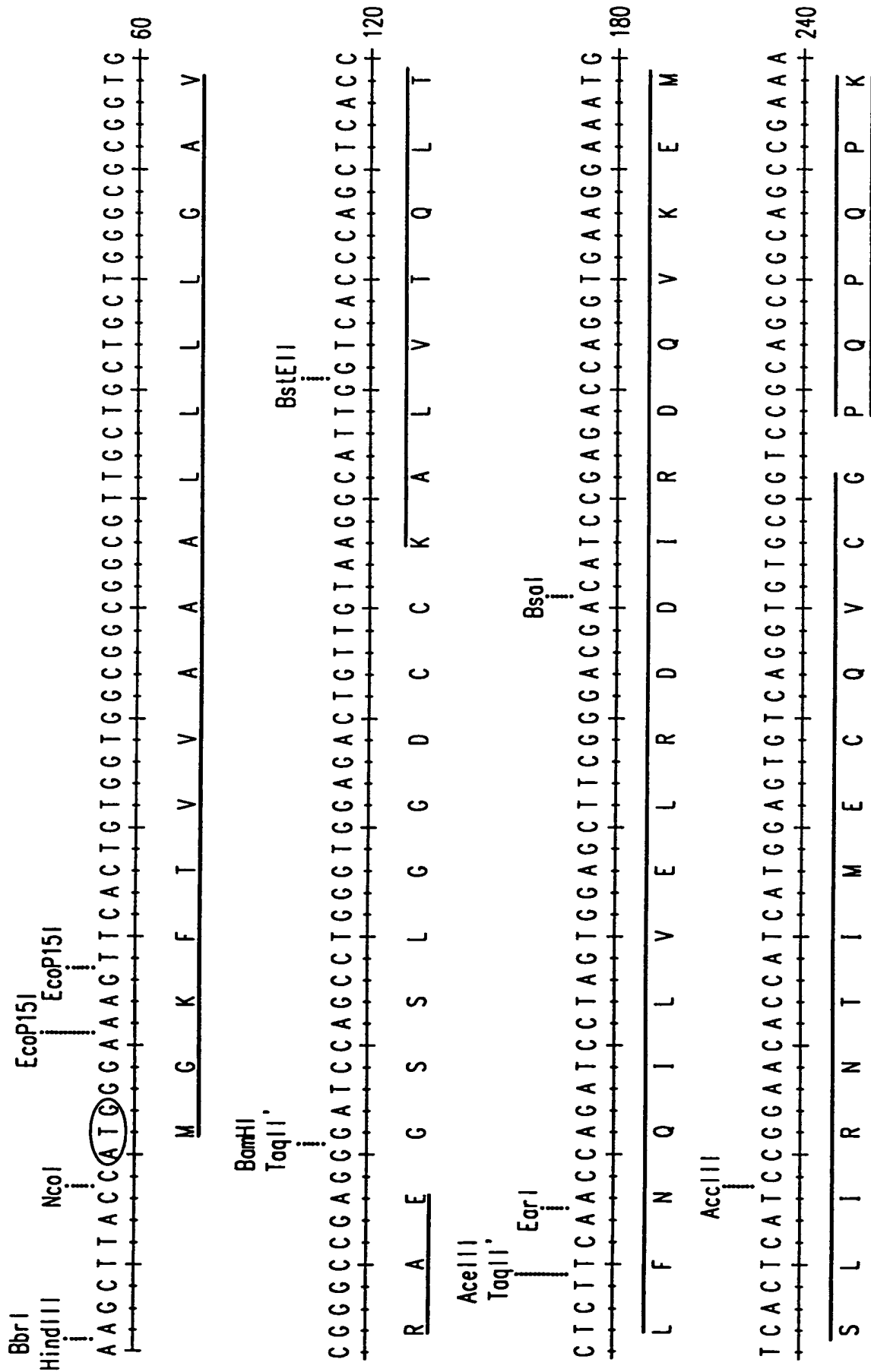


FIG. 3C



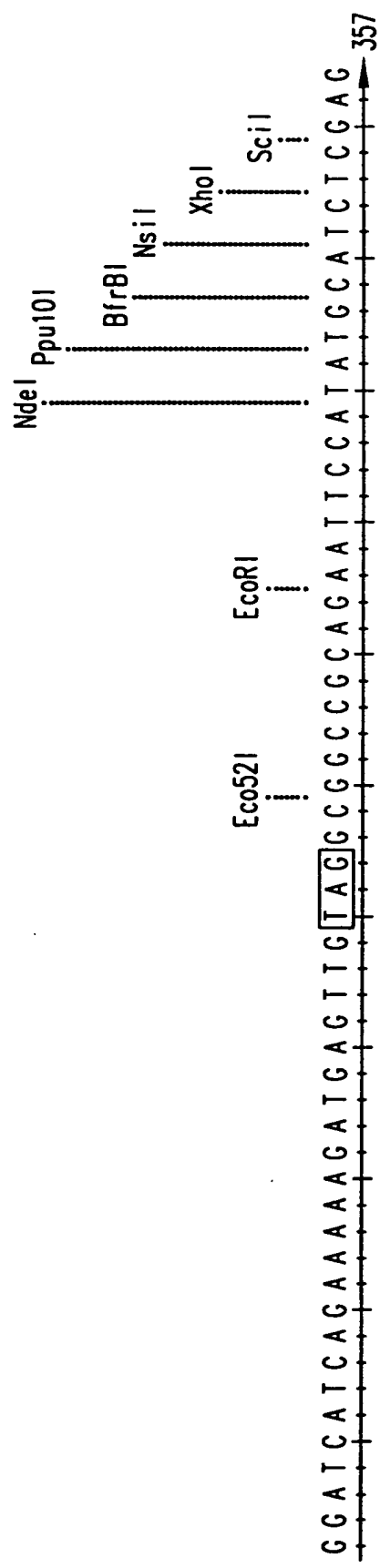
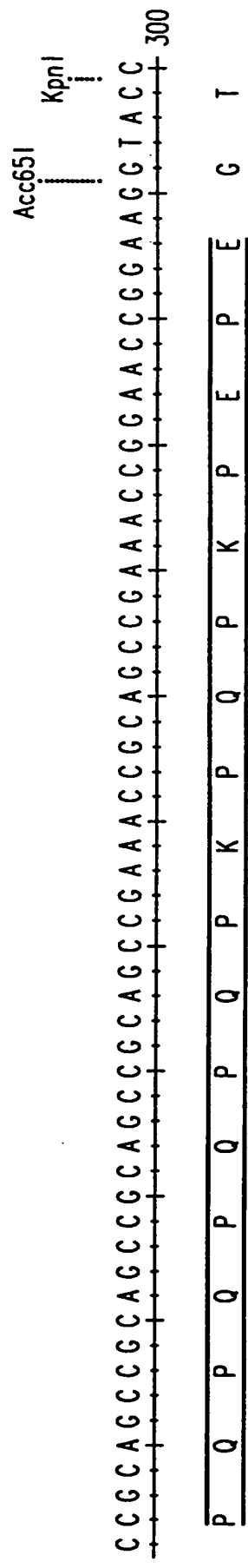


FIG. 3D



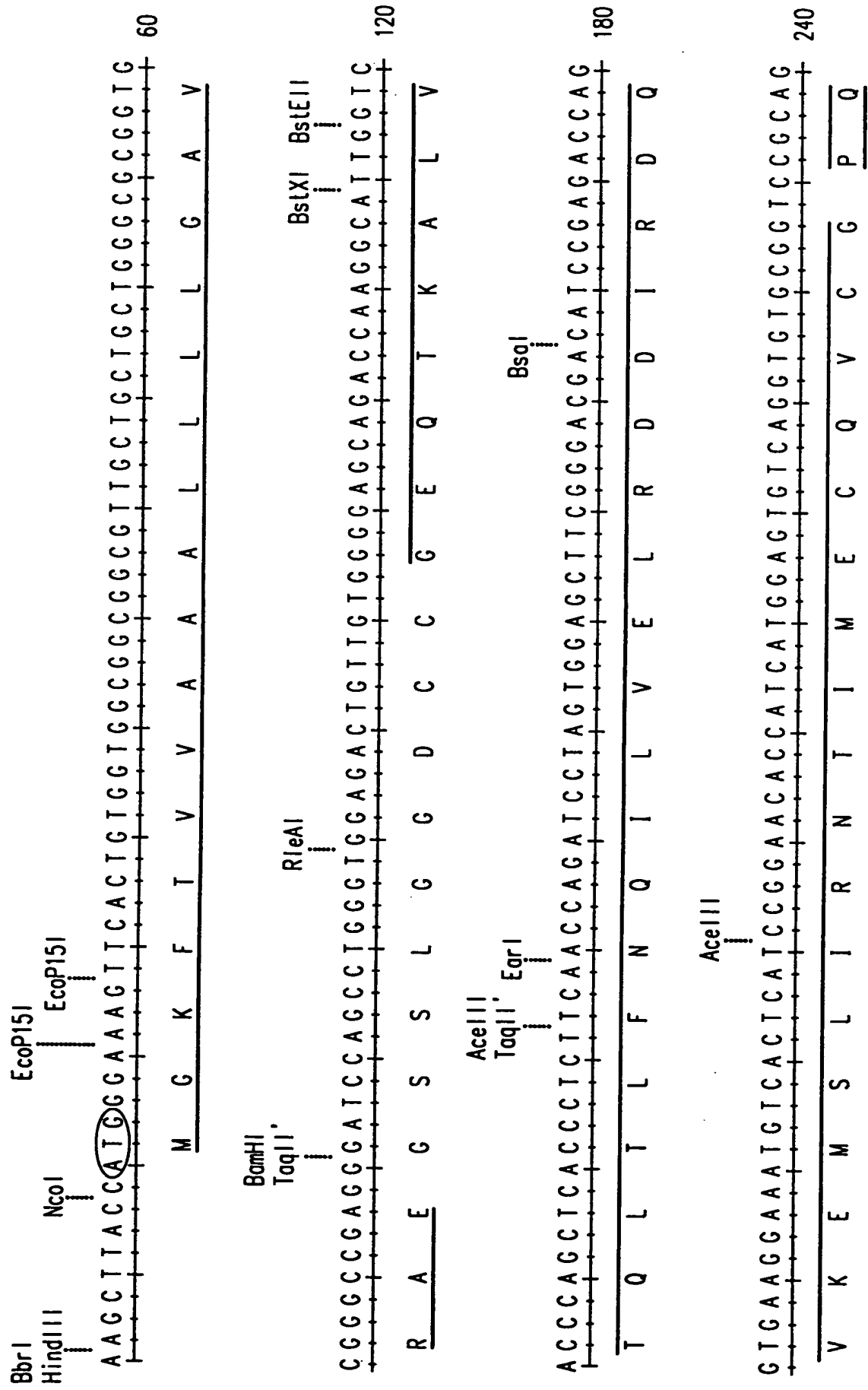


FIG. 4C



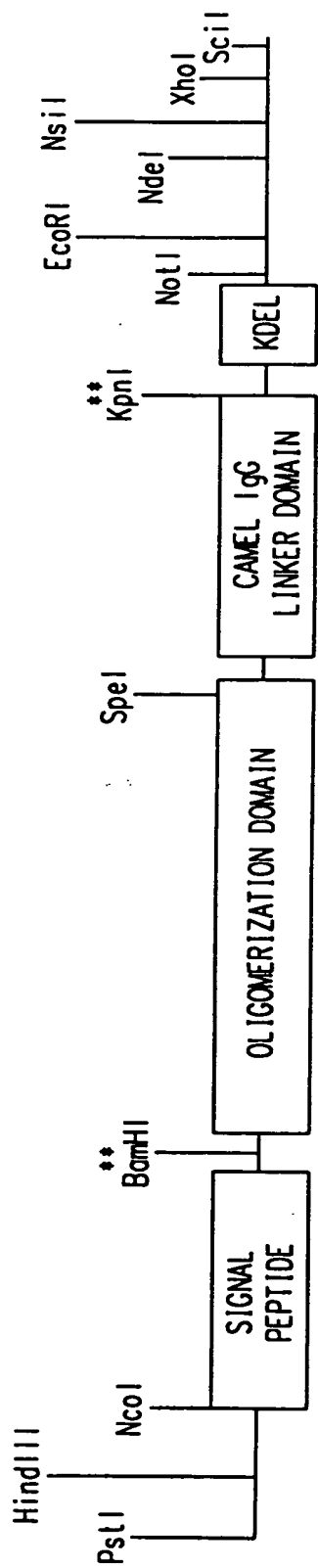


FIG. 5A

SIGNAL CLEAVAGE SITE

M G K F T V A A A L L L G A V R A E - G S S -

L G G D C C - G D V S R Q L I G Q I T Q M N Q M L G E L R D V M R Q Q V K E T M F L R N T I A E C Q A C G -

P Q P Q K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

FIG. 5B

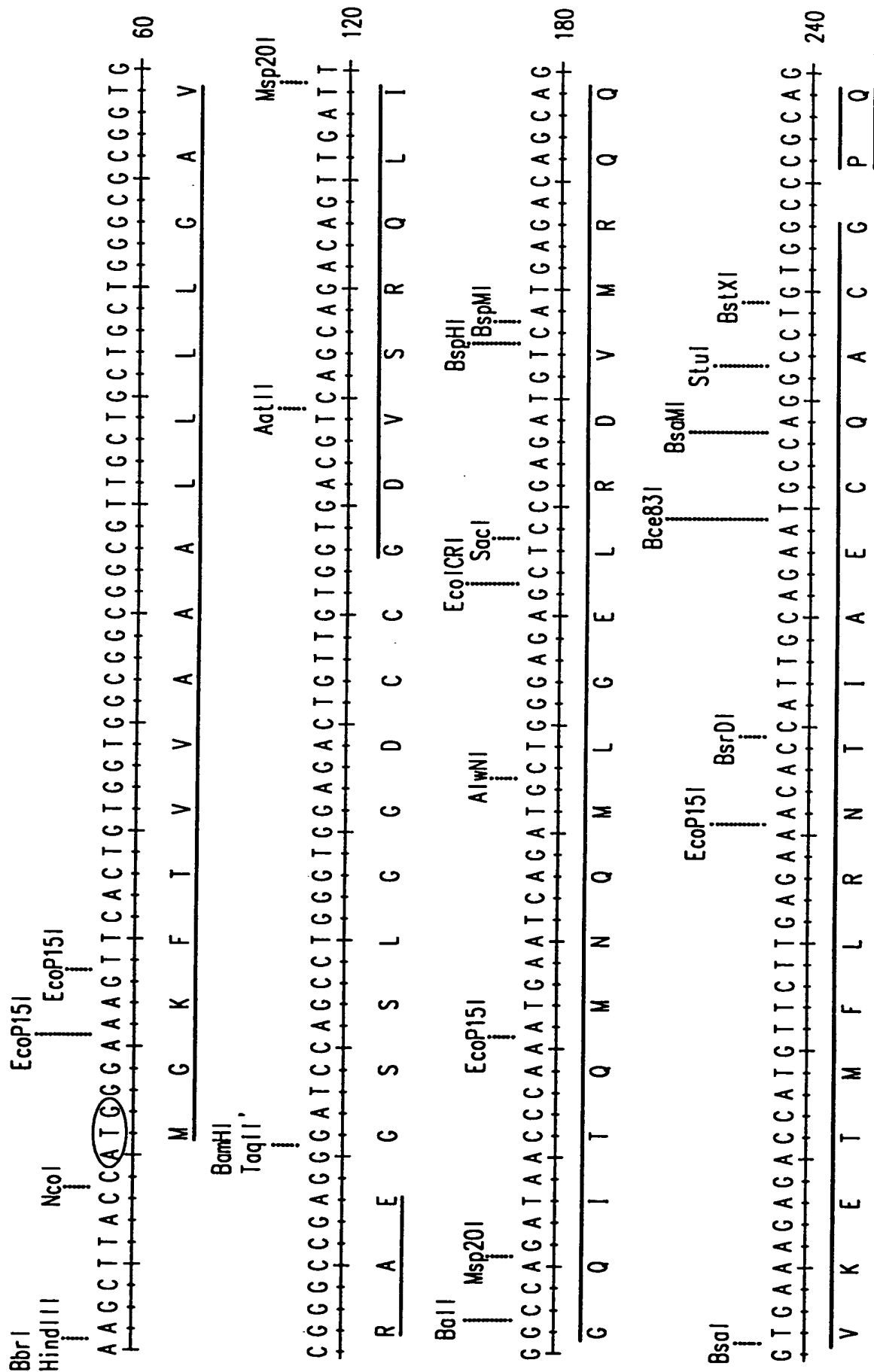


FIG. 5C



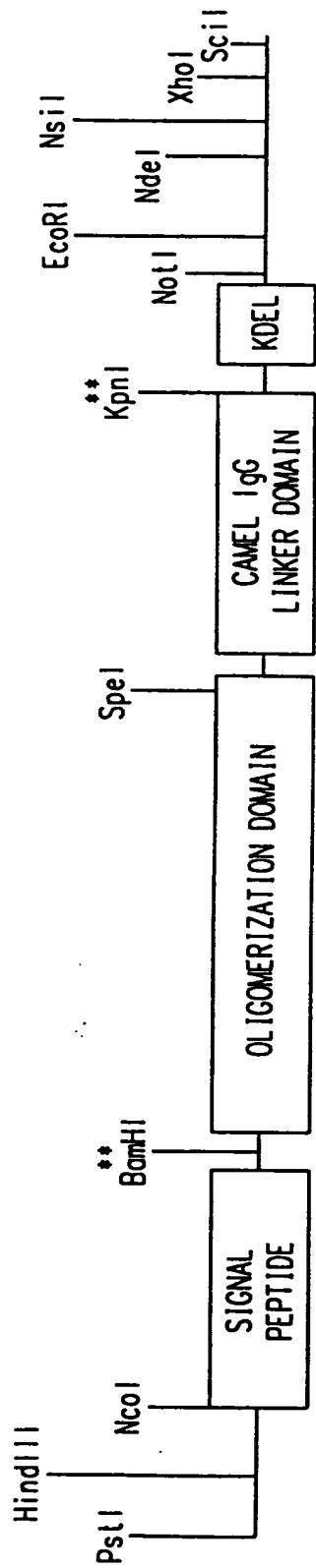


FIG. 6A

SIGNAL CLEAVAGE SITE

MRYMILGLLALAAVCSAAKK-GSS-

LGGDCC-SDLCPQMLRELQETNAALQDVRDWLRQQVREITFLKNTVMECDACG-

PQPQKPQPQPQPQPQKPEPE-GTGSSE-KDEL

FIG. 6B



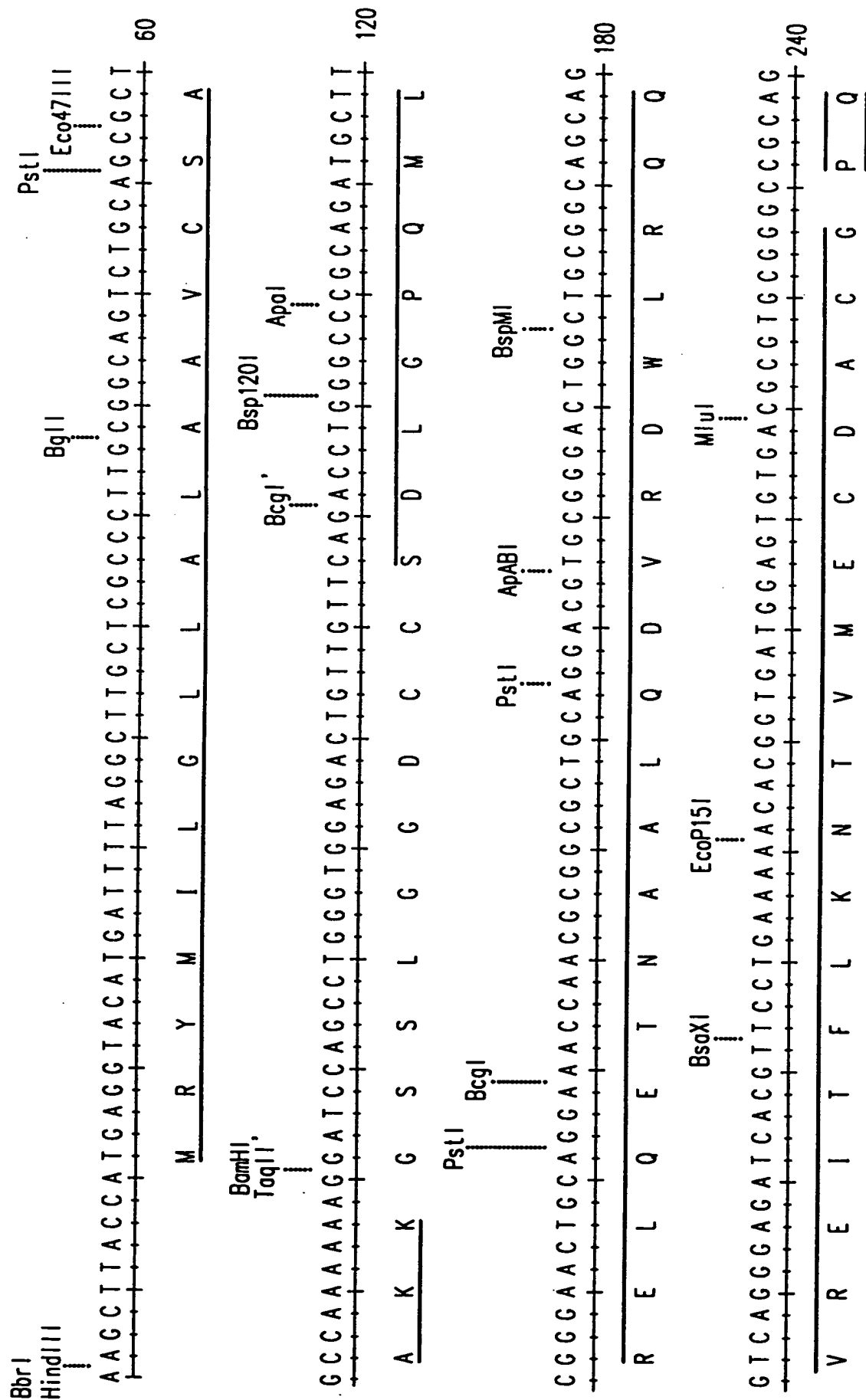


FIG. 6C

P Q P K P Q P Q P Q P Q P Q P Q P E

CCGGAAGGTACCGGATCATCAGAAAGATGAGTTGTAGCGCGCCGACGAATTC CATATC  
 NdeI Ppu10I Bfr8I  
 Eco52I EcoRI  
 KpnI Acc65I  
 360

P E G T G S S E X D E L .

A diagram of a DNA sequence: CATCTCGAG. Above the sequence, three restriction sites are indicated by vertical lines: NsiI at the first position (C), XhoI between the second and third positions (T and C), and SclI between the sixth and seventh positions (G and A). An arrow at the end of the sequence points to the right, labeled with the number 369.

**FIG. 6D**

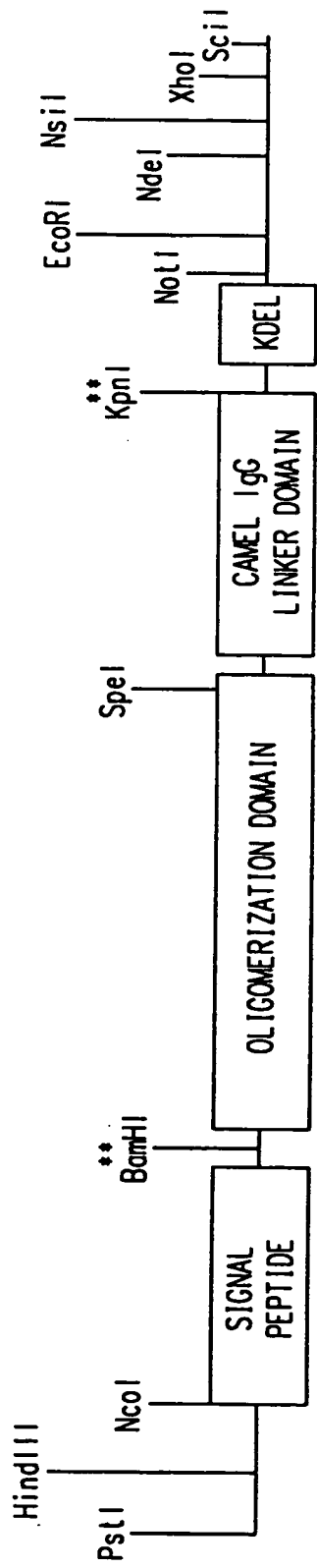


FIG. 7A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - Q K L Q N L F I N F C I I L I C L L I C I I V M L L -

P Q P Q K P Q P Q P Q P K P Q P K P E P E - G T G S S E - K D E L

• RESIDUES CRITICAL FOR PENTAMER FORMATION

FIG. 7B

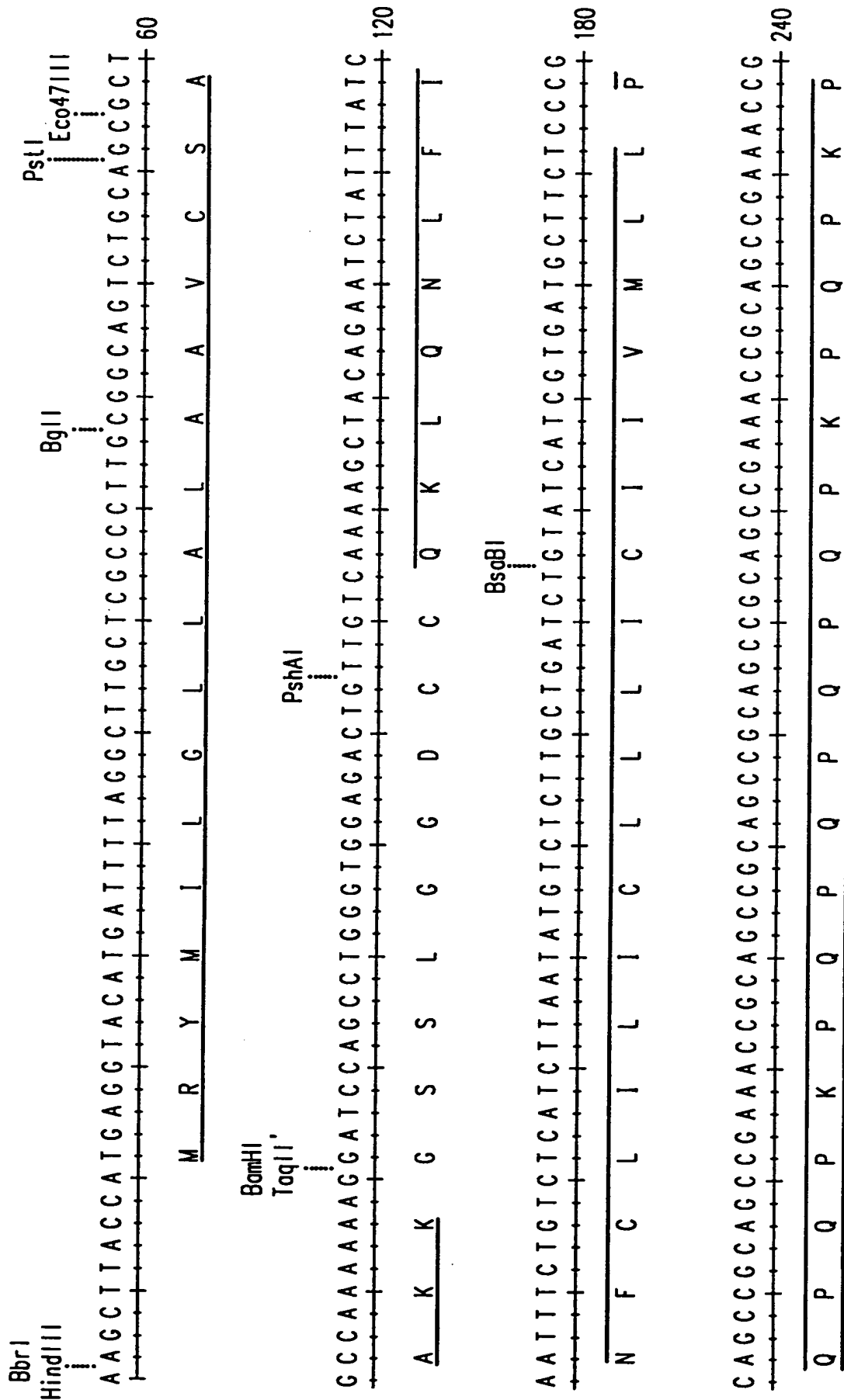


FIG. 7C

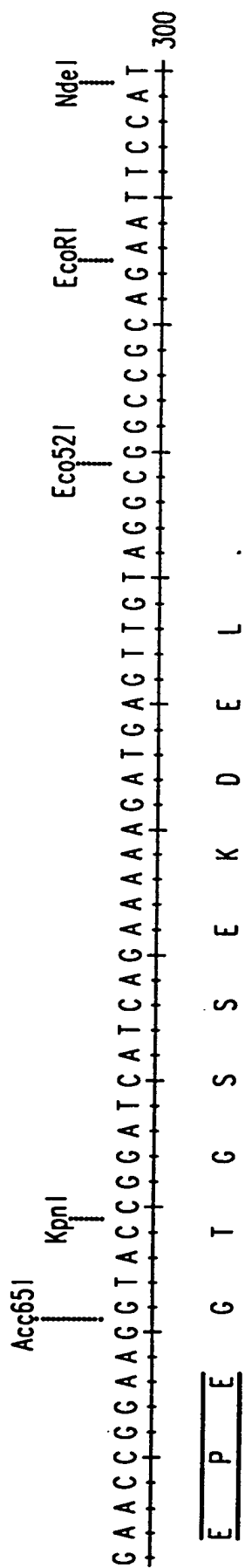
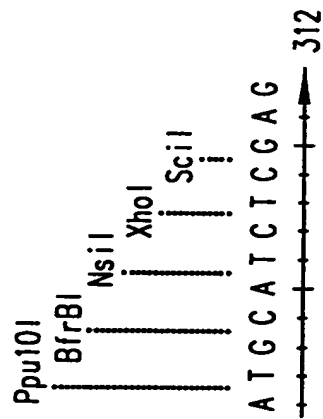
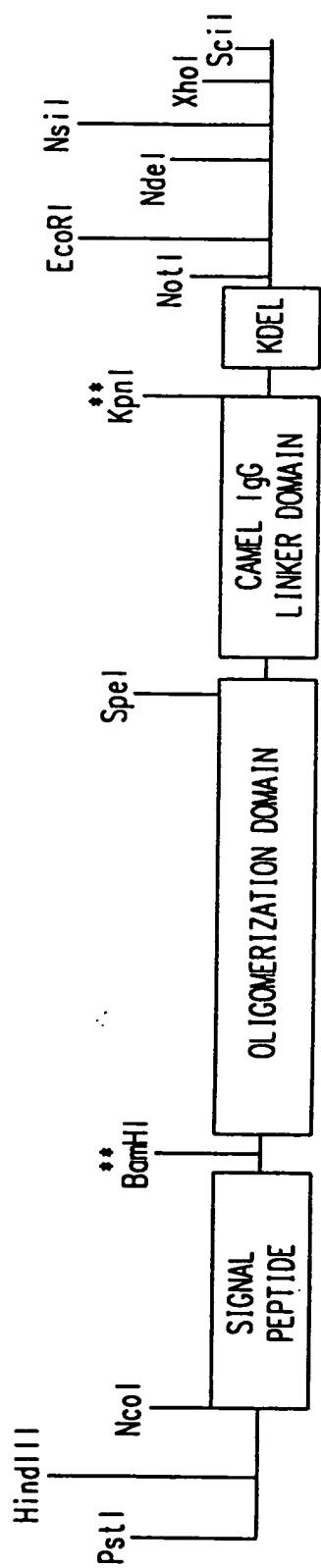


FIG. 7D





**FIG. 8A**

**SIGNAL CLEAVAGE SITE**

MRYMILGLLALA A VCSAAKK-GSS-

LGDDCC-GEQTKALVTQLTLFNQILVELRDDIRDQVKEMSLIRNTIMECQVCG-

PQPQKPQPQPQPQPQPQPQPQPQPQPQPQPQPQP-GTGSSE-KDEL

**FIG. 8B**

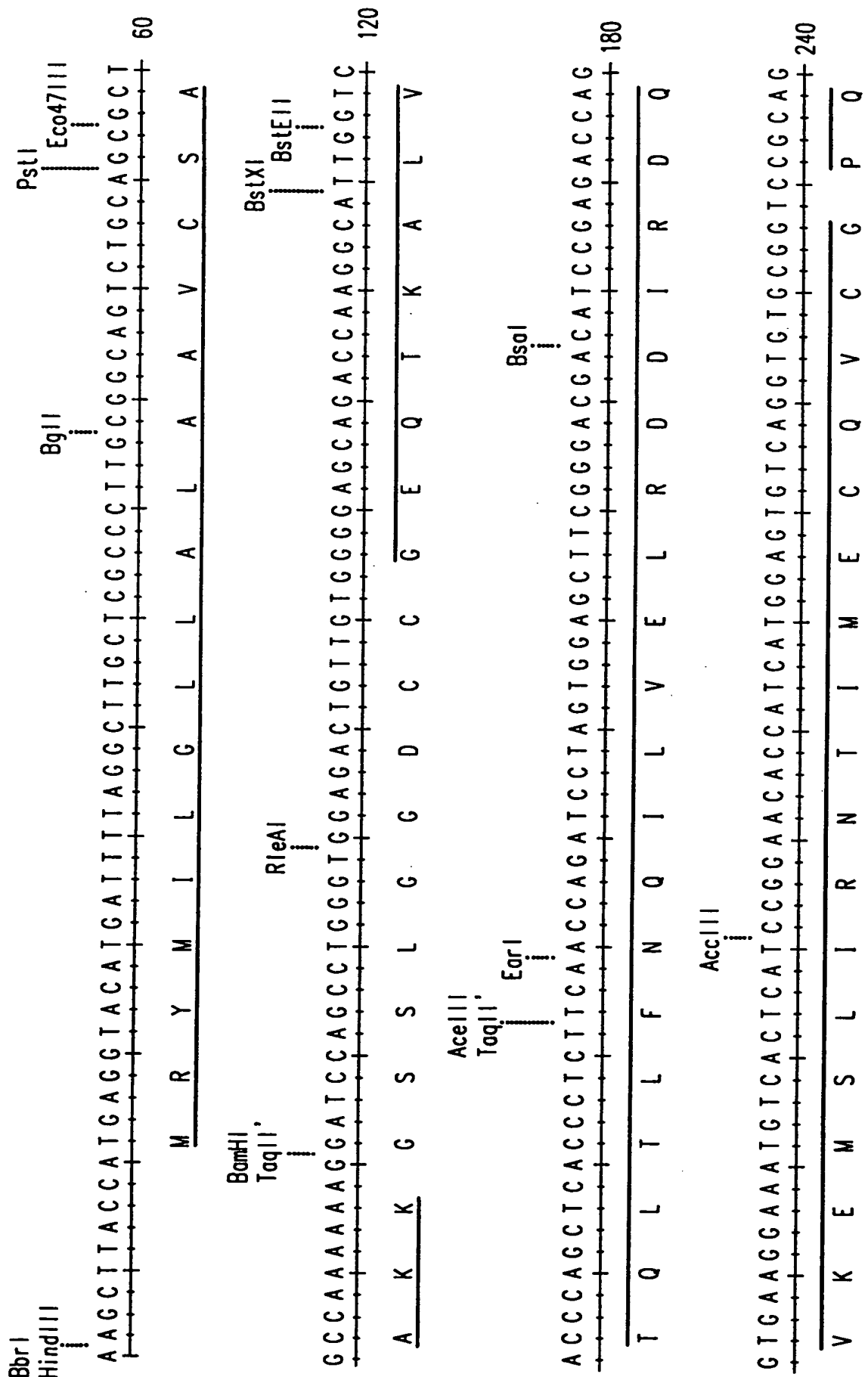


FIG. 8C

P	Q	P	K	P	Q	P	Q	P	Q	P	Q	P	Q	P	E
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

CCGGAAGGTACCGGATCATCAGAAAGATGAGTTGTAGCCGCCGACAAATTC CATATC  
 NdeI Ppu10I BfrBI  
 EcoRI  
 Eco52I  
 KpnI  
 Acc65I  
 360

PE G T G S S E K D E L .

Diagram illustrating the restriction enzyme sites for NsiI, XhoI, and SclI on the DNA sequence CATCTCGAG. The NsiI site is located at the beginning of the sequence, followed by the XhoI site, and then the SclI site. The sequence ends with the codon CAG, which is labeled as 369.

**FIG. 8D**



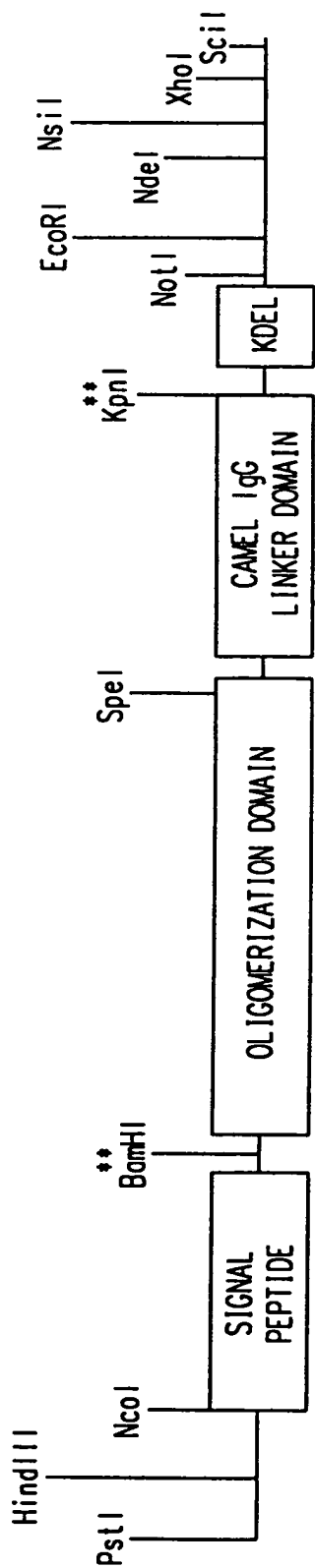


FIG. 9A

SIGNAL CLEAVAGE SITE

M R Y M I L G L L A L A A V C S A A K K - G S S -

L G G D C C - G D F N R Q F L G Q M T Q L N Q L L G E V K D L L R Q Q V K E T S F L R N T I A E C Q A C G -

P Q P Q P K P Q P Q P Q P Q P K P E P E - G T G S S E - K D E L

FIG. 9B

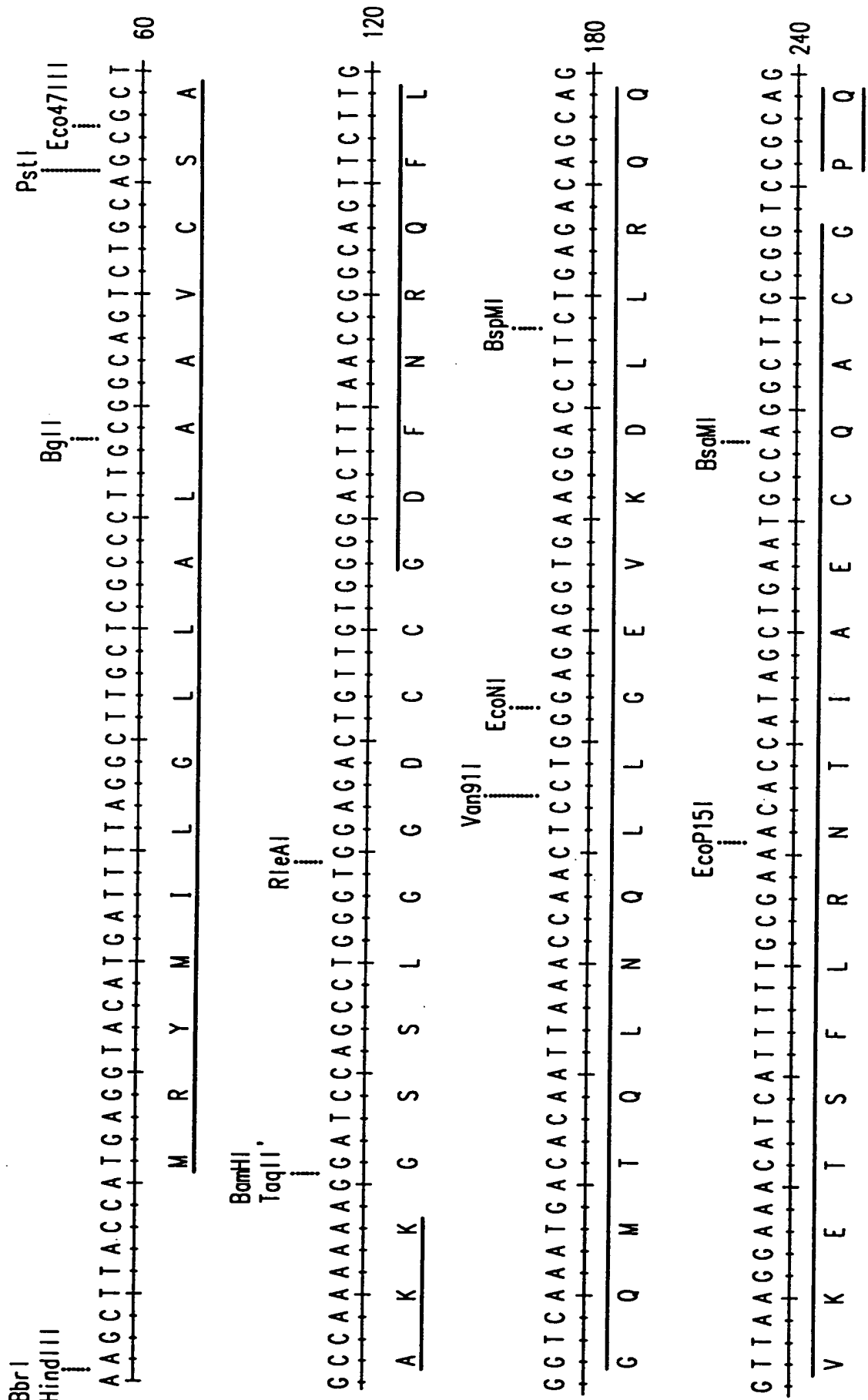


FIG. 9C

CCGCAGCCGAAACCCGAGCCGCGCAGCCGCAACCCGAGCCGCAACCCGGA 300

P Q P K P Q P Q P Q P Q P Q P K P Q P K P E

+

CCGGAAGGTACCGGATCATCAGAAAGAATGAGTTGTAGCGCGCCGAGAAATTCATATG 360

Acc65I KpnI NdeI Ppu10I BfrBI Eco52I EcoRI

P E G T G S S E K D E L .

NsiI XhoI SclI CATCTCGAG 369

FIG. 9D



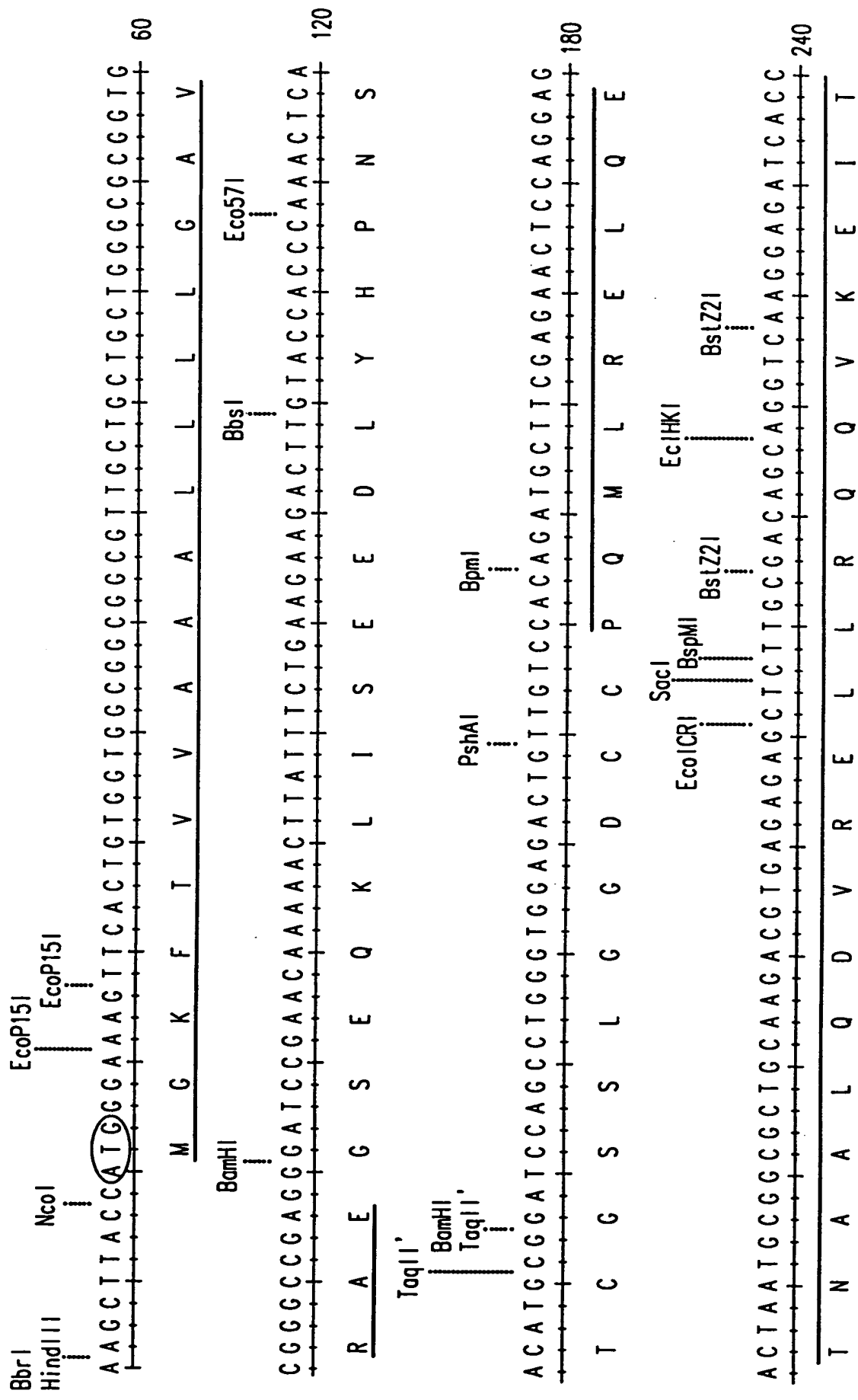


FIG. 10C

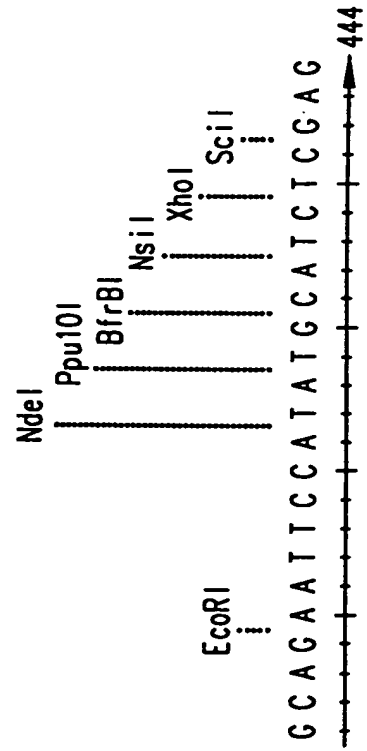
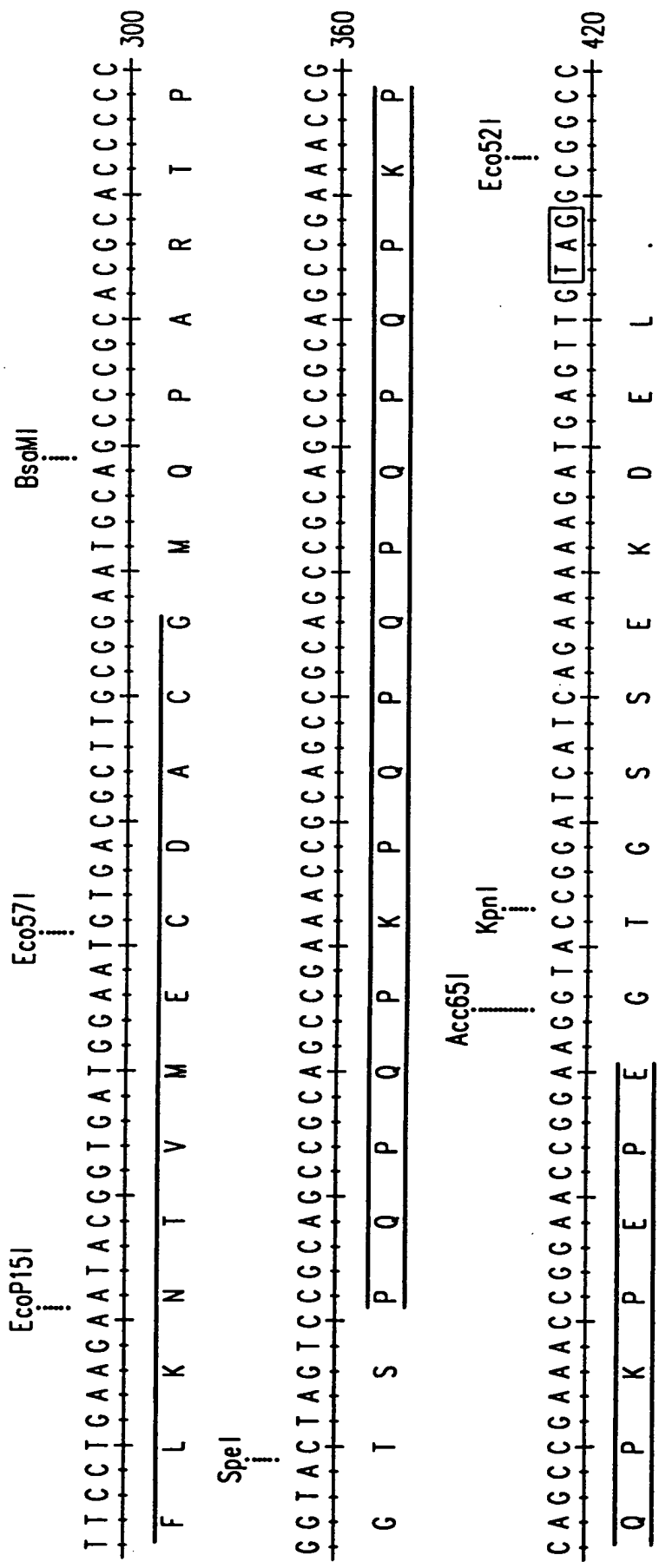


FIG. 10D